--4. [AMENDED] The method of claim 1 [any one of claims 1 to 3], wherein in step c) and/or d) the adaptor or primer used contains at least one phosphorothioate bond.--

--5. [AMENDED] The method of claim 1 [any one of claims 1 to 4], wherein step e) is performed using as primers, either successively or together, both the mixture of 5'-flanking VNTR amplimers and the mixture of 3'-flanking VNTR amplimers.--

--6. [AMENDED] The method of claim 1 [any one of claims 1 to 5], wherein there is used in step e) genomic DNA of one or more members of the species of interest which manifest a trait of interest, whereby the resulting mixture of VNTR alleles and their flanking sequences is representative of those which manifest the trait of interest.--

--9. [AMENDED] The method of claim 6 [any one of claims 6 to 8], wherein at least one VNTR allele and its flanking sequences representative of those which manifest the trait of interest, is hybridised with a mixture of VNTR alleles and their flanking sequences representative of those which do not manifest the trait of interest, and at least one match and/or at least one mis-match is selected to provide at least one VNTR allele or fragment thereof which is characteristic of the trait of interest.--

--13. [AMENDED] The portion as claimed in claim 11 [or claim 12], wherein each member of the mixture has an adaptor at each of its 3'-end and its 5'-end.--

--15. A portion of genomic DNA of a species of interest, said portion consisting essentially of a representative mixture of 3'-flanking regions of a chosen VNTR sequence, each member of the mixture carrying an adaptor at its 3'-end, and a representative mixture of 5'-flanking regions of a chosen VNTR sequence, each member of the mixture carrying the same [an] adaptor at its 5'-end.--

--19. [AMENDED] The method of claim 16 [any one of claims 16 to 18], wherein at least one VNTR allele and its flanking sequence representative of those which manifest the trait of interest, is hybridised with a mixture of VNTR alleles and their flanking sequences representative of those which do not manifest the trait of interest, and at least one match and/or at least one mis-match is selected to provide at least one VNTR allele or fragment thereof which is characteristic of the trait of interest.--

--24. [AMENDED] The method of claim 22 [or claim 23], wherein the at least one allele and its flanking sequences representative of those which manifest the trait of interest, is provided with 3'-overlapping ends.--

--26. [AMENDED] The method of claim 1 or claim 16 [claims 1 to 10 or 16 to 20], wherein the VNTR allele and its flanking regions, or the mixture of VNTR alleles and their flanking regions, is analysed by being applied under hybridsation conditions to an array of immobilised VNTR alleles and/or their flanking regions.--

--27. [AMENDED] A kit comprising protocols and reagents for performing the method of claim 1 or claim 16 or claim 24 [any one of claims 1 to 10, 16 to 24 or 26].